OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/963,668

DATE: 10/10/2001
TIME: 10:56:12

Input Set : A:\000425 BTe AL1_Dpckaec.app
Output Set: N:\CRF3\10102001\I963668.raw

Does Not Comply
Corrected Diskette Needed

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 3 <110> APPLICANT: Degussa AG
 5 <120> TITLE OF INVENTION: Process for the fermentative preparation of
 6       L-amino acids using strains of the
 7       Enterobacteriaceae family.
 9 <130> FILE REFERENCE: 000425 BT
11 <140> CURRENT APPLICATION NUMBER: US/09/963,668
12 <141> CURRENT FILING DATE: 2001-09-27
14 <160> NUMBER OF SEQ ID NOS: 19
16 <170> SOFTWARE: PatentIn Ver. 2.1
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ERRORED SEQUENCES

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18 <210> SEQ ID NO: 1          1623 (p.3)
19 <211> LENGTH: 1622
20 <212> TYPE: DNA
21 <213> ORGANISM: Escherichia coli
23 <220> FEATURE:
24 <221> NAME/KEY: CDS
25 <222> LOCATION: (1)..(1620)
26 <223> OTHER INFORMATION: pckA
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30 Met Arg Val Asn Asn Gly Leu Thr Pro Gln Glu Leu Glu Ala Tyr Gly
31  1               5                  10                  15
33 atc agt gac gta cat gat atc gtt tac aac cca agc tac gac ctg ctg      96
34 Ile Ser Asp Val His Asp Ile Val Tyr Asn Pro Ser Tyr Asp Leu Leu
35                 20                  25                  30
37 tat cag gaa gag ctc gat ccg agc ctg aca ggt tat gag cgc ggg gtg     144
38 Tyr Gln Glu Glu Leu Asp Pro Ser Leu Thr Gly Tyr Glu Arg Gly Val
39             35                  40                  45
41 tta act aat ctg ggt gcc gtt gcc gtc gat acc ggg atc ttc acc ggt     192
42 Leu Thr Asn Leu Gly Ala Val Ala Val Asp Thr Gly Ile Phe Thr Gly
43     50                  55                  60
45 cgt tca cca aaa gat aag tat atc gtc cgt gac gat acc act cgc gat     240
46 Arg Ser Pro Lys Asp Lys Tyr Ile Val Arg Asp Asp Thr Thr Arg Asp
47 65                  70                  75                  80
49 act ttc tgg tgg gca gac aaa ggc aaa ggt aag aac gac aac aaa cct     288
50 Thr Phe Trp Trp Ala Asp Lys Gly Lys Gly Lys Asn Asp Asn Lys Pro
51                 85                  90                  95
53 ctc tct ccg gaa acc tgg cag cat ctg aaa ggc ctg gtg acc agg cag     336
54 Leu Ser Pro Glu Thr Trp Gln His Leu Lys Gly Leu Val Thr Arg Gln
55                100                 105                 110
57 ctt tcc ggc aaa cgt ctg ttc gtt gtc gac gct ttc tgt ggt gcg aac     384
58 Leu Ser Gly Lys Arg Leu Phe Val Val Asp Ala Phe Cys Gly Ala Asn
59             115                 120                 125
62 ccg gat act cgt ctt tcc gtc cgt ttc atc acc gaa gtg gcc tgg cag     432
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63 Pro Asp Thr Arg Leu Ser Val Arg Phe Ile Thr Glu Val Ala Trp Gln
64       130             135             140
66 gcg cat ttt gtc aaa aac atg ttt att cgc ccg agc gat gaa gaa ctg   480
67 Ala His Phe Val Lys Asn Met Phe Ile Arg Pro Ser Asp Glu Glu Leu
68 145.            150             155             160
70 gca ggt ttc aaa cca gac ttt atc gtt atg aac ggc gcg aag tgc act   528
71 Ala Gly Phe Lys Pro Asp Phe Ile Val Met Asn Gly Ala Lys Cys Thr
72             165             170             175
74 aac ccg cag tgg aaa gaa cag ggt ctc aac tcc gaa aac ttc gtg gcg   576
75 Asn Pro Gln Trp Lys Glu Gln Gly Leu Asn Ser Glu Asn Phe Val Ala
76             180             185             190
78 ttt aac ctg acc gag cgc atg cag ctg att ggc ggc acc tgg tac ggc   624
79 Phe Asn Leu Thr Glu Arg Met Gln Leu Ile Gly Gly Thr Trp Tyr Gly
80             195             200             205
82 ggc gaa atg aag aaa ggg atg ttc tcg atg atg aac tac ctg ctg ccg   672
83 Gly Glu Met Lys Lys Gly Met Phe Ser Met Met Asn Tyr Leu Leu Pro
84       210             215             220
86 ctg aaa ggt atc gct tct atg cac tgc tcc gcc aac gtt ggt gag aaa   720
87 Leu Lys Gly Ile Ala Ser Met His Cys Ser Ala Asn Val Gly Glu Lys
88 225             230             235             240
90 ggc gat gtt gcg gtg ttc ttc ggc ctt tcc ggc acc ggt aaa acc acc   768
91 Gly Asp Val Ala Val Phe Phe Gly Leu Ser Gly Thr Gly Lys Thr Thr
92             245             250             255
94 ctt tcc acc gac ccg aaa cgt cgc ctg att ggc gat gac gaa cac ggc   816
95 Leu Ser Thr Asp Pro Lys Arg Arg Leu Ile Gly Asp Asp Glu His Gly
96             260             265             270
98 tgg gac gat gac ggc gtg ttt aac ttc gaa ggc ggc tgc tac gca aaa   864
99 Trp Asp Asp Asp Gly Val Phe Asn Phe Glu Gly Gly Cys Tyr Ala Lys
100        275             280             285
102 act atc aag ctg tcg aaa gaa gcg gaa cct gaa atc tac aac gct atc   912
103 Thr Ile Lys Leu Ser Lys Glu Ala Glu Pro Glu Ile Tyr Asn Ala Ile
104       290             295             300
106 cgt cgt gat gcg ttg ctg gaa aac gtc acc gtg cgt gaa gat ggc act   960
107 Arg Arg Asp Ala Leu Leu Glu Asn Val Thr Val Arg Glu Asp Gly Thr
108 305             310             315             320
110 atc gac ttt gat gat ggt tca aaa acc gag aac acc cgc gtt tct tat  1008
111 Ile Asp Phe Asp Asp Gly Ser Lys Thr Glu Asn Thr Arg Val Ser Tyr
112             325             330             335
114 ccg atc tat cac atc gat aac att gtt aag ccg gtt tcc aaa gcg ggc  1056
115 Pro Ile Tyr His Ile Asp Asn Ile Val Lys Pro Val Ser Lys Ala Gly
116             340             345             350
118 cac gcg act aag gtt atc ttc ctg act gct gat gct ttc ggc gtg ttg  1104
119 His Ala Thr Lys Val Ile Phe Leu Thr Ala Asp Ala Phe Gly Val Leu
120             355             360             365
123 ccg ccg gtt tct cgc ctg act gcc gat caa acc cag tat cac ttc ctc  1152
124 Pro Pro Val Ser Arg Leu Thr Ala Asp Gln Thr Gln Tyr His Phe Leu
125       370             375             380
127 tct ggc ttc acc gcc aaa ctg gcc ggt act gag cgt ggc atc acc gaa  1200
128 Ser Gly Phe Thr Ala Lys Leu Ala Gly Thr Glu Arg Gly Ile Thr Glu
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129 385                    390                 395                  400
131 ccg acg cca acc ttc tcc gct tgc ttc ggc gcg gca ttc ctg tcg ctg    1248
132 Pro Thr Pro Thr Phe Ser Ala Cys Phe Gly Ala Ala Phe Leu Ser Leu
133                405                 410                 415
135 cac ccg act cag tac gca gaa gtg ctg gtg aaa cgt atg cag gcg gcg    1296
136 His Pro Thr Gln Tyr Ala Glu Val Leu Val Lys Arg Met Gln Ala Ala
137                420                 425                 430
139 ggc gcg cag gct tat ctg gtt aac act ggc tgg aac ggc act ggc aaa    1344
140 Gly Ala Gln Ala Tyr Leu Val Asn Thr Gly Trp Asn Gly Thr Gly Lys
141                435                 440                 445
143 cgt atc tcg att aaa gat acc cgc gcc att atc gac gcc atc ctc aac    1392
144 Arg Ile Ser Ile Lys Asp Thr Arg Ala Ile Ile Asp Ala Ile Leu Asn
145      450                 455                 460
147 ggt tcg ctg gat aat gca gaa acc ttc act ctg ccg atg ttt aac ctg    1440
148 Gly Ser Leu Asp Asn Ala Glu Thr Phe Thr Leu Pro Met Phe Asn Leu
149 465                    470                 475                  480
151 gcg atc cca acc gaa ctg ccg ggc gta gac acg aag att ctc gat ccg    1488
152 Ala Ile Pro Thr Glu Leu Pro Gly Val Asp Thr Lys Ile Leu Asp Pro
153                485                 490                 495
155 cgt aac acc tac gct tct ccg gaa cag tgg cag gaa aaa gcc gaa acc    1536
156 Arg Asn Thr Tyr Ala Ser Pro Glu Gln Trp Gln Glu Lys Ala Glu Thr
157                500                 505                 510
159 ctg gcg aaa ctg ttt atc gac aac ttc gat aaa tac acc gac acc cct    1584
160 Leu Ala Lys Leu Phe Ile Asp Asn Phe Asp Lys Tyr Thr Asp Thr Pro
161      515                 520                 525
163 gcg ggt gcc gcg ctg gta gcg gct ggt ccg aaa ctg taa          1623
164 Ala Gly Ala Ala Leu Val Ala Ala Gly Pro Lys Leu
E--> 165     530                 535                 540
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VERIFICATION SUMMARY   DATE: 10/10/2001
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L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:165 M:252 E: No. of Seq. differs, <211>LENGTH:Input:1622 Found:1623 SEQ:1

Creation date: 01-28-2004
Indexing Officer: SSISOUVONG - SOURYACHANH SISOUVONG
Team: OIPEBackFileIndexing
Dossier: 09963668

Legal Date: 06-21-2002

No.	Doccode	Number of pages
1	IDS	1
2	NPL	1
3	NPL	7
4	NPL	1
5	NPL	9
6	NPL	1
7	NPL	3

Total number of pages: 23

Remarks:

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